Shipment Protocol Sequencing Services
Smarter_2_Nextera Flex

It is important to follow the criteria summarized below when sending RNA samples for Smarter_2_Nextera Flex Sequencing services to the Genomics Core Facility of Erasmus MC.

RNA Purity, Format and Quality Guidelines

1. The RIN values and concentrations (ng/uL) should be determined with Bioanalyzer.
2. The RIN values should be >8.0.
3. The sample volume should be >4 uL
4. The concentration should be >0.5 ng/uL
5. Hand in your samples undiluted. If diluting is required, we'll do the dilution.
   Leftover intake sample volume, will be returned at your request
6. Please make sure the RNA is free of RNAses, salts, metal ions, and organic solvents.
7. RNA samples should be aspirated in 1.5 mL and RNAse free LoBind safelock tubes.

   Make sure the identifiers on the tubes are clearly readable.

Cells input, Quality Guidelines

The input for this protocol can also be cells.

1. In case of cells please measure the amount of cells.
2. Calculate the nanograms of RNA the cells are supposed to yield (ES cells: 0.8-1.2 pg per cell; MEFs 4.8 – 4.9 pg per cell)
3. Hand in enough of the cellpellet to reach 1 ng RNA.
4. Cellpellets should be in 1.5 ml and RNAse free LoBind safelock tubes.

Sample Information File (SIF)

We'd like to receive an Excel Sample Information File (SIF) containing the following information for each sample:

1. The prep method ("Smarter RNA v2_Nextera Flex NS")
2. Analysis type (e.g. "NextSeq2000 PE50", see contract for details)
3. Tube ID

4. Sample name
5. Expected concentration (ng/uL)
6. Volume of the sample (uL)
7. Type of start material: (“Total RNA”or ”cells” (and what cells))
8. Species
9. Mapping reference (example: human (GRCh38); Mouse (GRCm38)

Please save this file with your contract number and prepmethod in the filename!
(e.g. SIF_S-2023-79_ Smarter_2_Nextera_Flex.xlxs)

Important considerations for sample IDs

For efficient processing of your samples, we recommend you to keep a few guidelines in mind concerning sample IDs. Most genetic software are unable to handle sample IDs including these features and will generate errors. Also tracking systems and Excel might recode sample IDs with these features. It is fixable post data-generation but this is error prone. When making your sample IDs please avoid the following:

- Special characters in sample IDs (e.g., 12.34 or 12,34 or 12_34 should be 1234)
- Spaces in sample IDs (e.g., 12 34 should be 1234)
- Number IDs starting with one or multiple ‘0’s (e.g., 01234 should be either 1234 or a01234)
- Duplicate IDs. If a sample has been run twice please add an addition to the IDs (e.g., 1234a and 1234b)

In general we advise to use a combination of numbers and letters, and avoid special characters, symbols and spaces.

Sample Shipping Guidelines

(external shipments)

1. Before sending samples, please contact our lab and send Sample Information File to: genomics-sequencing@erasmusmc.nl.
2. Make sure the tubes/plates are labeled with an Tube ID or Plate ID . Preferably use stickers.
3. Accompany the samples by the following information :
    - Contract number
    - Which samples should be present in the box
    - Research Centre / study name
4. RNA samples should be ***securely sealed, wrapped and shipped on dry ice*** by overnight courier. Do not ship samples on a Thursday, Friday or Saturday. Only ship samples after our lab has agreed on the moment of shipping.
5. Ship to the following address (open 7.30-16.30 hr):

        Erasmus MC

Genomics Core Facility
Att: <Name Technician> / <Contact Person>
Room Ee-575
Westzeedijk 353
3015 AA Rotterdam
The Netherlands

6. Please keep close contact with our lab at (see Contact information) when shipping the samples. Report exact time, date, shipment number etc. before sending the samples. We will notify you upon receiving the samples.

(internal shipments)

1. Before sending samples, please return a copy of your signed contract to get a project number.
2. Go to the website and log in using your account: https://biomics.erasmusmc.nl/wordpress/login/illumina-intake-2/
3. Select the corresponding project and fill in the required details of your samples.
4. After the sample registration, your samples are assigned to:
    - An Intake ID (I25-xxxx-xx)
    - A storage box position.
5. Bring your samples to Ee691; here you can find the printed labels, add the matching labels onto your samples.
6. Place the samples in the box (at the indicated positions) located in the “Intake” drawer of freezer 211.
7. Notify one of the technicians that you have delivered your samples, they will bring the RNA samples to the -80°C freezer.

Contact information

Mila Jhamai (Lab manager)
Erasmus MC
Genomics Core Facility
Room Ee-575
Westzeedijk 353
3015 AA Rotterdam
The Netherlands

Phone: +31(10) 7043645 (Mila Jhamai)

Email: p.jhamai@erasmusmc.nl
genomics-sequencing@erasmusmc.nl

For general questions regarding projects, please contact the contract- and project manager dr. Gaby van Dijk (g.m.vandijk@erasmusmc.nl or genomics@erasmusmc.nl).